

EXHIBIT

A

Query= SEQ ID NO:9 (PE 027-999)
(277 letters)



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Sequences producing significant alignments:

	Score	E
	(bits)	Value

AC020728.4.1.201404	539	e-151
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>AC020728.4.1.201404
Length = 201404

Score = 539 bits (272), Expect = e-151
Identities = 276/277 (99%), Gaps = 1/277 (0%)
Strand = Plus / Minus

Query: 1 gtgttgctgctgatgcaggagacaaccgcgaagatggggacagaatcagtaacatcgacgt 60
|||||
Sbjct: 77342 gtgttgctgctgatgcaggagacaaccgcgaagatggggacagaatcagtaacatcgacgt 77283

Query: 61 aagggaattgaagcagaagatcacgctgcctgcagacaccaggaaacgccaagaccccc 120
|||||
Sbjct: 77282 aagggaattgaagcagaagatcacgctgcctgcagacaccaggaaacgccaagaccccc 77223

Query: 121 ttccacgaaccaacattcttccaccctctccaaactttttctggaaccccttcactcca 180
|||||
Sbjct: 77222 ttccacgaaccaacattcttccaccctctccaaactttttctggaaccccttcactcca 77163

Query: 181 accgccactcaatgtacacttcactttctcgtgctcttctctaagagagtagtggtttctt 240
|||||
Sbjct: 77162 a-cgccactcaatgtacacttcactttctcgtgctcttctctaagagagtagtggtttctt 77104

Query: 241 cctccccaccgagaaaaaaaataaaagcaacaactgg 277
|||||
Sbjct: 77103 cctccccaccgagaaaaaaaataaaagcaacaactgg 77067

Query= SEQ ID NO:10 (PE 027-999)
(434 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
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AL035467	402	e-109
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>AL035467 ACCESSION:AL035467 NID: gi 6522967 emb AL035467.23 HS288M22
Human DNA sequence from clone RP1-288M22 on chromosome
6q12-13, complete sequence
Length = 155960

Score = 402 bits (203), Expect = e-109
Identities = 218/220 (99%), Gaps = 1/220 (0%)
Strand = Plus / Minus

Query: 215 ttctctaggttaagcctggatggagcctctaagacctaacaggatgtctgagattccaggg 274
|||||
Sbjct: 79194 ttctctaggtatgcctggatggagcctctaagacctaacaggatgtctgagattccaggg 79135

Query: 275 aagtggcctgtgatctgtcagtaaacaaaataagaagctaatacagctttgttgtgttttc 334
|||||
Sbjct: 79134 aagtggcctgtgatctgtcagtaaacaaaataagaagctaatacagctttgttgtgttttc 79075

Query: 335 tgattggcatgggttcctgaactatctcctactttagttgcagacaaagaaacaggagat 394
|||||
Sbjct: 79074 tgattggcatgggttc-tgaactatctcctactttagttgcagacaaagaaacaggagat 79016

Query: 395 gaattaccatgttctaggactttgtgttcctttccaattc 434
|||||
Sbjct: 79015 gaattaccatgttctaggactttgtgttcctttccaattc 78976

Score = 242 bits (122), Expect = 8e-61
Identities = 122/122 (100%)
Strand = Plus / Minus

Query: 1 cgctcatgttctctgcaaaagagaaaaataaggaaaaaatctgcaaaacattgaagactcatg 60
|||||
Sbjct: 82893 cgctcatgttctctgcaaaagagaaaaataaggaaaaaatctgcaaaacattgaagactcatg 82834

Query: 61 acccactttaaaaacataactggatacatcacatgaactcaagaccatgactatggagga 120
|||||
Sbjct: 82833 acccactttaaaaacataactggatacatcacatgaactcaagaccatgactatggagga 82774

Query: 121 ag 122
||
Sbjct: 82773 ag 82772

Score = 186 bits (94), Expect = 4e-44
Identities = 94/94 (100%)
Strand = Plus / Minus

Query: 121 agatttaacacttggcaactcttacaacaacaacacagcaacagggaaaaacaaca 180
|||||
Sbjct: 82642 agatttaacacttggcaactcttacaacaacaacacagcaacagggaaaaacaaca 82583

Query: 181 acaacaaccgaagagtgcaaaaagaactaatgca 214
|||||
Sbjct: 82582 acaacaaccgaagagtgcaaaaagaactaatgca 82549

Query= SEQ ID NO:11 (PE 027-999)
(407 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AC099759.4.1.101955	<u>771</u>	0.0
AC005061.2.1.114828	<u>771</u>	0.0

>AC099759.4.1.101955
Length = 101955

Score = 771 bits (389), Expect = 0.0
Identities = 389/389 (100%)
Strand = Plus / Plus

Query: 1 gttcacaaacagtgttatggcgggagcagggaggcacctacatccattggacccatcctga 60
|||||
Sbjct: 70683 gttcacaaacagtgttatggcgggagcagggaggcacctacatccattggacccatcctga 70742

Query: 61 cagctgggaaggatgtgtccagccacccagggatgtgcatctggcaccacctcacaaca 120
|||||
Sbjct: 70743 cagctgggaaggatgtgtccagccacccagggatgtgcatctggcaccacctcacaaca 70802

Query: 121 gctgtttctaaccacgtaagaagcacaaaggtcaccggttactctccatgagaacaaaagg 180
|||||
Sbjct: 70803 gctgtttctaaccacgtaagaagcacaaaggtcaccggttactctccatgagaacaaaagg 70862

Query: 181 ccaaggatgcagagataattgcatcaaaggattcaacttcctggatgacctcattccaa 240
|||||
Sbjct: 70863 ccaaggatgcagagataattgcatcaaaggattcaacttcctggatgacctcattccaa 70922

Query: 241 agatctgcagagcccagataaagcatcccagggttctggcagagggccctccagggacag 300
|||||
Sbjct: 70923 agatctgcagagcccagataaagcatcccagggttctggcagagggccctccagggacag 70982

Query: 301 gaaggggacaggaagccggctttccgtgtctgtaccgccttccttgggaaggataggaca 360
|||||
Sbjct: 70983 gaaggggacaggaagccggctttccgtgtctgtaccgccttccttgggaaggataggaca 71042

Query: 361 cctgtggccatcaagtcatgatgccccat 389
|||||
Sbjct: 71043 cctgtggccatcaagtcatgatgccccat 71071

>AC005061.2.1.114828
Length = 114828

Score = 771 bits (389), Expect = 0.0
Identities = 389/389 (100%)
Strand = Plus / Plus

Query: 1 gttcacacaagtggttatggcgggagcaggaggcacctacatccattggacccatcctga 60
|||||
Sbjct: 52921 gttcacacaagtggttatggcgggagcaggaggcacctacatccattggacccatcctga 52980

Query: 61 cagctgggaaggatgtgtccagccacccagggtgtgcatctggcaccacctcacaaca 120
|||||
Sbjct: 52981 cagctgggaaggatgtgtccagccacccagggtgtgcatctggcaccacctcacaaca 53040

Query: 121 gctgttctaaccacgtaagaagcaccaagggtcaccggttactctccatgagaacaaaagg 180
|||||
Sbjct: 53041 gctgttctaaccacgtaagaagcaccaagggtcaccggttactctccatgagaacaaaagg 53100

Query: 181 ccaaggatgcagagataattgcatcaaagggttcaacttcctggatgacctcattccaa 240
|||||
Sbjct: 53101 ccaaggatgcagagataattgcatcaaagggttcaacttcctggatgacctcattccaa 53160

Query: 241 agatctgcagagcccagataagcatcccagggttctggcagagggccctccagggacag 300
|||||
Sbjct: 53161 agatctgcagagcccagataagcatcccagggttctggcagagggccctccagggacag 53220

Query: 301 gaaggggacaggaagccggctttccgtgtctgtaccgccttccttgggaaggataggaca 360
|||||
Sbjct: 53221 gaaggggacaggaagccggctttccgtgtctgtaccgccttccttgggaaggataggaca 53280

Query: 361 cctgtggccatcaagtcatgatgccccat 389
|||||
Sbjct: 53281 cctgtggccatcaagtcatgatgccccat 53309

Query= SEQ ID NO:12 (PE 027-999)
(200 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL034548.25.1.153170	<u>389</u>	e-106

>AL034548.25.1.153170
Length = 153170

Score = 389 bits (196), Expect = e-106
Identities = 199/200 (99%)
Strand = Plus / Minus

Query: 1 gaggagaactggtggctttataagaagaggaagagagaccaaagcatagcatgtcagcat 60
|||||
Sbjct: 131570 gaggagaactggtggctttataagaagaggaagagagaccaaagcatagcatgtcagcat 131511

Query: 61 gccccagtcacctctccacgctataacctgtgccacctccagacacttcagagaccaggaa 120
|||||
Sbjct: 131510 gccccagtcacctctccacgctataacctgtgccacctccagacacttcagagaccaggaa 131451

Query: 121 taaggccctcaccagaagtgccccctcaatcttggacttcctatcctccatggctgtaag 180
|||||
Sbjct: 131450 taaggccctcaccagaagtgccccctcaatcttggacttcctatcctccatagctgtaag 131391

Query: 181 gaataaatccctttctttc 200
|||||
Sbjct: 131390 gaataaatccctttctttc 131371

Query= SEQ ID NO:13 (PE 027-999)
(128 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AP002006.5.1.167355	254	1e-65
AP001981.5.1.183476	254	1e-65

>AP002006.5.1.167355
Length = 167355

Score = 254 bits (128), Expect = 1e-65
Identities = 128/128 (100%)
Strand = Plus / Minus

Query: 1 atgaagggaaaagagggagaagaaccagctgcctggaagactgacctctgagatgctct 60
|||||
Sbjct: 65476 atgaagggaaaagagggagaagaaccagctgcctggaagactgacctctgagatgctct 65417

Query: 61 ggagccgtgcagttgttctcactggcagatcagtcctgtccctccaataaaagagaggggt 120
|||||
Sbjct: 65416 ggagccgtgcagttgttctcactggcagatcagtcctgtccctccaataaaagagaggggt 65357

Query: 121 gatcttgg 128
|||||
Sbjct: 65356 gatcttgg 65349

>AP001981.5.1.183476
Length = 183476

Score = 254 bits (128), Expect = 1e-65
Identities = 128/128 (100%)
Strand = Plus / Minus

Query: 1 atgaagggaaaagagggagaagaaccagctgcctggaagactgacctctgagatgctct 60
|||||
Sbjct: 6771 atgaagggaaaagagggagaagaaccagctgcctggaagactgacctctgagatgctct 6712

Query: 61 ggagccgtgcagttgttctcactggcagatcagtcctgtccctccaataaaagagaggggt 120
|||||
Sbjct: 6711 ggagccgtgcagttgttctcactggcagatcagtcctgtccctccaataaaagagaggggt 6652

Query: 121 gatcttgg 128
|||||
Sbjct: 6651 gatcttgg 6644

Query= SEQ ID NO:14 (PE 027-999)
(142 letters)

Sequences producing significant alignments:

Score E
(bits) Value

AC008536.7.1.178056

281 5e-74

>AC008536.7.1.178056

Length = 178056

Score = 281 bits (142), Expect = 5e-74

Identities = 142/142 (100%)

Strand = Plus / Minus

Query: 1 ctgaaagcaaagaactcttttagatagtgaggctcacactggaaaaagcacagacccttgag 60
|||||
Sbjct: 112260 ctgaaagcaaagaactcttttagatagtgaggctcacactggaaaaagcacagacccttgag 112201

Query: 61 tgtactgcttggaggagagctaccctggagcatttgctccagattctgcatgagcaaaaa 120
|||||
Sbjct: 112200 tgtactgcttggaggagagctaccctggagcatttgctccagattctgcatgagcaaaaa 112141

Query: 121 ataaacttttgctgcataaagt 142
|||||
Sbjct: 112140 ataaacttttgctgcataaagt 112119

Query= SEQ ID NO:15 (PE 027-999)
(149 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC073576	<u>295</u>	2e-77
AL355916	<u>295</u>	2e-77

>AC073576 ACCESSION:AC073576 NID: gi 15055235 gb AC073576.23 Homo sapiens
12 BAC RP11-363M20 (Roswell Park Cancer Institute Human BAC
Library) complete sequence
Length = 180309

Score = 295 bits (149), Expect = 2e-77
Identities = 149/149 (100%)
Strand = Plus / Plus

Query: 1 acacttaatctgggtgttctctgaggctgacctattggaatatcttgctgaagaccacgtat 60
|||||
Sbjct: 163535 acacttaatctgggtgttctctgaggctgacctattggaatatcttgctgaagaccacgtat 163594

Query: 61 acaagatgtgaacattcatcattatgaggctgaatgtaaaatacttcattttataatgaa 120
|||||
Sbjct: 163595 acaagatgtgaacattcatcattatgaggctgaatgtaaaatacttcattttataatgaa 163654

Query: 121 gaaagtcagtaaaacaatttccagcccag 149
|||||
Sbjct: 163655 gaaagtcagtaaaacaatttccagcccag 163683

>AL355916 ACCESSION:AL355916 NID: g1 13928043 emb AL355916.2 CNS05TD1
Human chromosome 14 DNA sequence BAC R-47I22 of library
RPC1-11 from chromosome 14 of Homo sapiens (Human),
complete sequence
Length = 178484

Score = 295 bits (149), Expect = 2e-77
Identities = 149/149 (100%)
Strand = Plus / Plus

```
Query: 1      acacttaatctggtgttctgaggetgacctattggaatatcttgctgaagaccacgcat 60
             |||
Sbjct: 152230 acacttaatctggtgttctgaggetgacctattggaatatcttgctgaagaccacgcat 152289
```

```

Query: 61      acaagatgtgaacattcatcattatgaggctgaatgtaaaatacttcattttataatgaa 120
               |||
Sbjct: 152290 acaagatgtgaacattcatcattatgaggctgaatgtaaaatacttcattttataatgaa 152349

```

```
Query: 121      gaaagtcagtaaaacaatttcagcccag 149
               |||
Sbjct: 152350   gaaagtcagtaaaacaatttcagcccag 152378
```

Query= SEQ ID NO:17 (PE 027-999)
(113 letters)

Sequences producing significant alignments:

Score E
(bits) Value

AC091022.4.1.155949

161 1e-37

>AC091022.4.1.155949

Length = 155949

Score = 161 bits (81), Expect = 1e-37
Identities = 85/86 (98%), Gaps = 1/86 (1%)
Strand = Plus / Minus

Query: 28 aattatgagtcactaaaattatccaaaagatcattttaccgtaaagtagttgctgaatg 87
|||||
Sbjct: 48272 aattatgagtcactaaaattatccaaaagatcatttta-cgtaaagtagttgctgaatg 48214

Query: 88 tacacgaaatgttttagaaattaaatt 113
|||||
Sbjct: 48213 tacacgaaatgttttagaaattaaatt 48188

Query= SEQ ID NO:18 (PE 027-999)
(250 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
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AF440620	<u>484</u>	e-134
AL158195	<u>484</u>	e-134
AC005949	<u>476</u>	e-131

>AF440620 ACCESSION:AF440620 NID: gi 16580084 gb AF440620.1 AF440620 Homo
sapiens 13q14 chronic lymphocytic leukemia suppressor locus
section 2 of 2
Length = 440917

Score = 484 bits (244), Expect = e-134
Identities = 248/250 (99%)
Strand = Plus / Minus

Query: 1 cttctnctgaagaatgagaacacttgccagccctttgcctatgttatcacctggaataaa 60
|||||
Sbjct: 106753 cttctcctgaagaatgagaacacttgccagccctttgcctatgttatcacctggaataaa 106694

Query: 61 ctggatgtgtctnaatggaacctgcctcctttggggagcgcatactcccgccaggtcacc 120
|||||
Sbjct: 106693 ctggatgtgtctaaatggaacctgcctcctttggggagcgcatactcccgccaggtcacc 106634

Query: 121 acagccaccatgaccacctcatgcctcccatccacctgtttcattaatttgcgctggac 180
|||||
Sbjct: 106633 acagccaccatgaccacctcatgcctcccatccacctgtttcattaatttgcgctggac 106574

Query: 181 cattttcagttttcttggatgacatgggtgaggaggaggaaactcaggtaaatgataaagt 240
|||||
Sbjct: 106573 cattttcagttttcttggatgacatgggtgaggaggaggaaactcaggtaaatgataaagt 106514

Query: 241 ttcgactatc 250
|||||
Sbjct: 106513 ttcgactatc 106504

>AL158195 ACCESSION:AL158195 NID: gi 11182170 emb AL158195.11 Human DNA
sequence from clone RP11-48H1 on chromosome 13 Contains
STSS and GSSs, complete sequence
Length = 123209

Score = 484 bits (244), Expect = e-134
Identities = 248/250 (99%)
Strand = Plus / Minus

Query: 1 cttctnctgaagaatgagaacacttgccagccctttgcctatgttatcacctggaataaa 60
|||||
Sbjct: 28043 cttctcctgaagaatgagaacacttgccagccctttgcctatgttatcacctggaataaa 27984
|||||

Query: 61 ctggatgtgtctnaatggaacctgcctcctttggggagcgcatactcccgccaggtcacc 120
|||||
Sbjct: 27983 ctggatgtgtctaaatggaacctgcctcctttggggagcgcatactcccgccaggtcacc 27924
|||||

Query: 121 acagccaccatgaccacctcatgcctcccatccacctgtttcattaatttgtgcctggac 180
|||||
Sbjct: 27923 acagccaccatgaccacctcatgcctcccatccacctgtttcattaatttgtgcctggac 27864
|||||

Query: 181 cattttcagttttctggatgacatgggtgaggaggaggaaactcaggtaaatgataaagt 240
|||||
Sbjct: 27863 cattttcagttttctggatgacatgggtgaggaggaggaaactcaggtaaatgataaagt 27804
|||||

Query: 241 ttcgactatc 250
|||||
Sbjct: 27803 ttcgactatc 27794
|||||

```
>AC005949 ACCESSION:AC005949 NID: gi 6862981 gb AC005949.12 Homo sapiens
      chromosome 13 clone 468p13 map 13q14, complete sequence
      Length = 143107
```

Score = 476 bits (240), Expect = e-131
Identities = 247/250 (98%)
Strand = Plus / Plus